

Amendments to the Claims:

1. (previously presented) An isolated nucleic acid comprising a nucleotide sequence having at least 90% sequence identity to the nucleotide sequence set forth in SEQ ID NO:1, wherein said nucleotide sequence encodes a polypeptide which is pesticidal for at least one pest belonging to the order Coleoptera.

2. (original) The nucleic acid according to claim 1, wherein the nucleotide sequence is optimized for expression in a plant.

3. (original) An expression cassette comprising a nucleic acid according to claim 1, wherein said nucleotide sequence is operably linked to a promoter that drives expression in a microorganism or in a plant cell.

4-8. (canceled)

9. (previously presented) A transformed plant comprising in its genome at least one stably incorporated nucleotide construct comprising a nucleotide sequence encoding a polypeptide operably linked to a promoter that drives expression of said polypeptide, wherein said polypeptide is pesticidal for at least one pest belonging to the order Coleoptera and wherein said nucleotide sequence has at least 90% sequence identity to the nucleotide sequence set forth in SEQ ID NO:1.

10. (original) The plant according to claim 9, wherein the plant is a monocot.

11. (original) The plant according to claim 9, wherein said plant is a dicot.

12. (original) Transformed seed of the plant according to claim 9.

13-16. (canceled)

17. (previously presented) A method for impacting an insect pest comprising introducing into a plant or cell thereof at least one nucleotide construct comprising a nucleotide sequence encoding a polypeptide operably linked to a promoter that drives expression of said polypeptide in plant cells, wherein said polypeptide is pesticidal for at least one pest belonging to the order Coleoptera and wherein said nucleotide sequence has at least 90% sequence identity to the nucleotide sequence set forth in SEQ ID NO:1, whereby an insect pest feeding on said plant or cell thereof is impacted.

18. (previously presented) The method according to claim 17, wherein the plant produces a polypeptide characterized by pesticidal activity against at least one pest of the order Coleoptera.

19. (previously presented) The method according to claim 18, wherein said insect pest is selected from the group consisting of Colorado potato beetle, western corn rootworm, southern corn rootworm, and boll weevil.

20-37. (canceled)

38. (previously presented) The nucleic acid of claim 1, wherein said nucleotide sequence has at least 95% identity to the nucleotide sequence set forth in SEQ ID NO:1.

39. (previously presented) The nucleic acid of claim 1, wherein said nucleotide sequence encodes the amino acid sequence set forth in SEQ ID NO:2.

40. (previously presented) The nucleic acid of claim 1, wherein said nucleotide sequence is set forth in SEQ ID NO:1.

41. (canceled)

42. (currently amended) A first nucleotide sequence that hybridizes under stringent conditions to a nucleic acid consisting of the second nucleotide sequence set forth in SEQ ID NO:1, wherein said first nucleotide sequence encodes a polypeptide which is pesticidal for at least one pest belonging to the order Coleoptera and wherein said stringent conditions include hybridization for 12 hours in 50% formamide, 1M NaCl, and 1% SDS at 37°C, and a wash in 0.1x SSC at 4°C lower than the thermal melting point of the hybrid of said first nucleotide sequence and said second nucleotide sequence, wherein said thermal melting point is between 60°C to 65°C.

43. (previously presented) The transformed plant of claim 9, wherein said nucleotide sequence has at least 95% identity to the nucleotide sequence set forth in SEQ ID NO:1.

44. (previously presented) The transformed plant of claim 9, wherein said nucleotide sequence encodes the amino acid sequence set forth in SEQ ID NO:2.

45. (previously presented) The transformed plant of claim 9, wherein said nucleotide sequence is set forth in SEQ ID NO:1.

46. (previously presented) The transformed plant of claim 9, wherein said nucleotide sequence is optimized for expression in a plant.

47. (canceled)

48. (currently amended) A transformed plant comprising in its genome at least one stably incorporated nucleotide construct comprising a first nucleotide sequence that hybridizes under stringent conditions to a nucleic acid consisting of the second nucleotide sequence set forth in SEQ ID NO:1, wherein said stringent conditions include hybridization for 12 hours in 50% formamide, 1M NaCl, and 1% SDS at 37°C, and a wash in 0.1x SSC at 4°C lower than the

thermal melting point of the hybrid of said first nucleotide sequence and said second nucleotide sequence, wherein said thermal melting point is between 60°C to 65°C.

49. (previously presented) The method of claim 17, wherein said nucleotide sequence has at least 95% identity to the nucleotide sequence set forth in SEQ ID NO:1.

50. (previously presented) The method of claim 17, wherein said nucleotide sequence encodes the amino acid sequence set forth in SEQ ID NO:2.

51. (previously presented) The method of claim 17, wherein said nucleotide sequence is set forth in SEQ ID NO:1.

52. (previously presented) The method of claim 17, wherein said nucleotide sequence is optimized for expression in a plant.

53. (canceled)

54. (currently amended) A method for impacting an insect pest comprising introducing into a plant or cell thereof at least one nucleotide construct comprising a first nucleotide sequence that hybridizes under stringent conditions to a nucleic acid consisting of the second nucleotide sequence set forth in SEQ ID NO:1, wherein said first nucleotide sequence encodes a polypeptide which is pesticidal for at least one pest belonging to the order Coleoptera and wherein said stringent conditions include hybridization for 12 hours in 50% formamide, 1M NaCl, 1% SDS at 37°C, and a wash in 0.1x SSC at 4°C lower than the thermal melting point of the hybrid of said first nucleotide sequence and said second nucleotide sequence, wherein said thermal melting point is between 60°C to 65°C.

55. (previously presented) The nucleic acid of claim 1, wherein said nucleotide sequence has at least 93% sequence identity to the nucleotide sequence set forth in SEQ ID NO:1.

56. (previously presented) The nucleic acid of claim 1, wherein said nucleotide sequence has at least 94% sequence identity to the nucleotide sequence set forth in SEQ ID NO:1.

57. (previously presented) The nucleic acid of claim 1, wherein said nucleotide sequence is optimized for expression in a plant.

58. (previously presented) The transformed plant of claim 9, wherein said nucleotide sequence has at least 93% sequence identity to the sequence set forth in SEQ ID NO:1.

59. (previously presented) The transformed plant of claim 9, wherein said nucleotide sequence has at least 94% sequence identity to the sequence set forth in SEQ ID NO:1.

60. (previously presented) The plant of claim 57, wherein said plant is a dicot.

61. (previously presented) The plant of claim 57, wherein said plant is a monocot.

62. (previously presented) The plant of claim 57, wherein said monocot is maize.

63. (previously presented) The method of claim 17, wherein said nucleotide sequence has at least 93% sequence identity to the sequence set forth in SEQ ID NO:1.

64. (previously presented) The method of claim 17, wherein said nucleotide sequence has at least 94% sequence identity to the sequence set forth in SEQ ID NO:1.